

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/552,909A
Source: IFWP
Date Processed by STIC: 11/7/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/552,909A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 J Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

RAW SEQUENCE LISTING

DATE: 11/07/2006

PATENT APPLICATION: US/10/552,909A

TIME: 11:51:44

Input Set : N:\RJAVED\10552909A.txt

Output Set: N:\CRF4\11072006\J552909A.raw

*see item 4 on Error
summary sheet*

supp 1, 3-4

**Does Not Comply
Corrected Diskette Needed**

*Since this is
a patent
document
number,
change
to
<3107>*

3 <110> APPLICANT: Xiao, Yingxao
4 Feng, Xin-Hua
6 <120> TITLE OF INVENTION: Gene expression suppression agents
8 <130> FILE REFERENCE: 132848-01US
10 <140> CURRENT APPLICATION NUMBER: US 10/552,909A
11 <141> CURRENT FILING DATE: 2005-10-13
13 <160> NUMBER OF SEQ ID NOS: 9
15 <210> SEQ ID NO: 1
16 <211> LENGTH: 27
17 <212> TYPE: DNA
18 <213> ORGANISM: Human
20 <220> FEATURE:
21 <221> NAME/KEY: primer_bind
22 <223> OTHER INFORMATION: Primer to amplify upstream promoter containing Box D in the
23 Human 5S RNA gene
W--> 25 <310> PATENT DOC NO: PCT/US2003/014631
26 <311> PATENT FILING DATE: 2003-05-12
W--> 27 <312> PUBLICATION DATE: PCT WO 2004/106488 A2
29 <400> SEQUENCE: 1
30 aacggatcca aaacgctgcc tccgcga 27
32 <210> SEQ ID NO: 2
33 <211> LENGTH: 25
34 <212> TYPE: DNA
35 <213> ORGANISM: Human
37 <220> FEATURE:
38 <221> NAME/KEY: primer_bind
39 <223> OTHER INFORMATION: Downstream reverse primer used to amplify the upstream
40 promoter containing Box D in the Human 5S RNA gene. The
41 sequence contains a PstI site at 7 bp upstream of the
42 transcription site.
44 <400> SEQUENCE: 2
45 tagacgctgc aggagcgcc tggct 25
51 <210> SEQ ID NO: 3
52 <211> LENGTH: 269
53 <212> TYPE: DNA
54 <213> ORGANISM: Human
56 <220> FEATURE:
57 <221> NAME/KEY: promoter
58 <223> OTHER INFORMATION: Calculated BamHI-PstI fragment of the upstream promoter
59 containing Box D in the Human 5S gene. Cloned into
60 pBluescript-KS to give plasmid pPPVI.
62 <400> SEQUENCE: 3
63 ggatccaaaa cgctgcctcc ggcacagggc ggaggacgga gggcgtccca ggatcgtggg 60

*<300> insert this numeric identifier
at the beginning of
publication information.
It never has a
response.*

*this is
for Publication Date
use this format: yyyy-mm-dd*

RAW SEQUENCE LISTING

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Input Set : N:\RJAVED\10552909A.txt

Output Set: N:\CRF4\11072006\J552909A.raw

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65 ccctgggcct gacgcctcgg agcactccct gctccgagcg ggcccgatgt ggtggaagct 120
67 cgggagcgcg ggagccgggg gaaggccgcg ggcagccgtc ggggggtcccc gatccgagcc 180
69 ccgcggcccc gggctggcgg tgcggctgc aatccggcgg gcacggccgg ccgggctggg 240
71 ctcttggggc agccaggcgc ctccttcag 269
73 <210> SEQ ID NO: 4
74 <211> LENGTH: 84
75 <212> TYPE: DNA
76 <213> ORGANISM: Human
78 <220> FEATURE:
79 <221> NAME/KEY: terminator
80 <223> OTHER INFORMATION: Comprises Box A, C and terminator of the human 5S RNA gene.
81     Serves as a top strand to anneal with SEQ ID NO: 5 to
82     create a double-stranded DNA molecule.
84 <400> SEQUENCE: 4
86 agaagacgaa gctaagcagg gtcgggcctg gttagtactt ggatgggaga ccgcctggga 60
88 ataccggtg ctgtaggctt ttg 84
91 <210> SEQ ID NO: 5
92 <211> LENGTH: 88
93 <212> TYPE: DNA
94 <213> ORGANISM: Human
96 <220> FEATURE:
97 <221> NAME/KEY: terminator
98 <223> OTHER INFORMATION: Comprises Box A, C and terminator of the human 5S RNA gene.
99     Serves as a top strand to anneal with SEQ ID NO: 4 to
100    create a double-stranded DNA molecule.
102 <400> SEQUENCE: 5
103 tcgacaaaaa gcctacagca cccggtattc ccaggcggtc tcccatccaa gtactaacca 60
105 ggcccgaccc tgcttagctt cgtcttct 88
108 <210> SEQ ID NO: 6
109 <211> LENGTH: 367
110 <212> TYPE: DNA
111 <213> ORGANISM: Human
113 <220> FEATURE:
114 <221> NAME/KEY: promoter
115 <223> OTHER INFORMATION: A BamHI-SalI fragment of plasmid pPPV2 containing the
116     upstream promoter containing Box D, A, C and the terminator
117     of the Human 5S gene.
119 <400> SEQUENCE: 6
120 ggatccaaaa cgctgcctcc gcgacagggc ggaggacgga gggcggtccca ggatcgtggg 60
122 ccctgggcct gacgcctcgg agcactccct gctccgagcg ggcccgatgt ggtggaagct 120
124 cgggagcgcg ggagccgggg gaaggccgcg ggcagccgtc ggggggtcccc gatccgagcc 180
126 ccgcggcccc gggctggcgg tgcggctgc aatccggcgg gcacggccgg ccgggctggg 240
128 ctcttggggc agccaggcgc ctccttcagg aattcgatag aagacgaagc taagcagggt 300
130 cgggcctggt tagtacttgg atgggagacc gcctgggaat accgggtgctg taggctttt 360
132 tgtcgac 367
134 <210> SEQ ID NO: 7
135 <211> LENGTH: 51
136 <212> TYPE: DNA
137 <213> ORGANISM: Human

```

RAW SEQUENCE LISTING

DATE: 11/07/2006

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Input Set : N:\RJAVED\10552909A.txt

Output Set: N:\CRF4\11072006\J552909A.raw

139 <220> FEATURE:
 140 <221> NAME/KEY: misc_RNA
 141 <223> OTHER INFORMATION: Contains designed siRNA sequence. Serves as a top strand
 142 to anneal with SEQ ID NO: 8 to create a double-stranded DNA
 143 molecule with PstI at the 5' end and BbsI at the 3' end.
 145 <400> SEQUENCE: 7
 W--> 146 gnnnnnnnnnn nnnnnnnnnn ntttcggnnn nnnnnnnnnn nnnnnntttt t 51
 149 <210> SEQ ID NO: 8
 150 <211> LENGTH: 59
 151 <212> TYPE: DNA
 152 <213> ORGANISM: Human
 154 <220> FEATURE:
 155 <221> NAME/KEY: misc_RNA
 156 <223> OTHER INFORMATION: Contains designed siRNA sequence. Serves as a top strand
 157 to anneal with SEQ ID NO: 7 to create a double-stranded DNA
 158 molecule with PstI at the 5' end and BbsI at the 3' end.
 160 <400> SEQUENCE: 8
 W--> 161 agctaaaaah nnnnnnnnnn nnnnnnnncc gaaannnnnnn nnnnnnnnnn nnnngctgca 59
 163 <210> SEQ ID NO: 9
 164 <211> LENGTH: 399
 165 <212> TYPE: DNA
 166 <213> ORGANISM: Human
 168 <220> FEATURE:
 169 <221> NAME/KEY: misc_structure
 170 <223> OTHER INFORMATION: A BamHI-SalI fragment of plasmid pPPV2 containing the siRNA
 171 design. The second stretch of the 19 "n" bases are
 172 complementary and reverse to the first stretch.
 174 <400> SEQUENCE: 9
 175 ggatccaaaa cgctgcctcc ggcacagggc ggaggacgga gggcgctcca ggatcgtggg 60
 177 ccctgggcct gacgcctcgg agcactccct gctccgagcg gggccgatgt ggtggaagct 120
 179 cgggagcgcg ggagccgggg gaaggccgcg ggcagccgctc ggggggtccc gatccgagcc 180
 181 ccgcggcccc gggtctggcg tctcggtctc aatccggcgg gcacggcccg ccgggctggg 240
 W--> 183 ctcttggggc agccaggcgc ctcttccagc nnnnnnnnnn nnnnnnnnt ttcggnnnnn 300
 185 nnnnnnnnnn nnnnttttta gctaagcagg gtcgggcctg gttagtactt ggatgggaga 360
 187 ccgcctggga ataccgggtg ctgtaggctt tttgtcgac 399

n's need
 explanation. see
 P. 4 for
 even
 explanation

see P. 4

OK, but all the n's
 need

explanation,
 further

which
 bases do
 these n's
 represent?

FYI: all nucleotides
 MUST be in
 lower-case
 letters

(see 1.823 of
 Sequence Rules)
 and P. 4

VARIABLE LOCATION SUMMARY

DATE: 11/07/2006

PATENT APPLICATION: US/10/552,909A

TIME: 11:51:45

Input Set : N:\RJAVED\10552909A.txt

Output Set: N:\CRF4\11072006\J552909A.raw

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which
residue n or Xaa represents.

Seq#:7; N Pos. 3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,28,29,30
Seq#:7; N Pos. 31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46
Seq#:8; N Pos. 10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,35
Seq#:8; N Pos. 36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53
Seq#:9; N Pos. 271,272,273,274,275,276,277,278,279,280,281,282,283,284,285
Seq#:9; N Pos. 286,287,288,289,296,297,298,299,300,301,302,303,304,305,306
Seq#:9; N Pos. 307,308,309,310,311,312,313,314

VERIFICATION SUMMARY

DATE: 11/07/2006

PATENT APPLICATION: US/10/552,909A

TIME: 11:51:45

Input Set : N:\RJAVED\10552909A.txt

Output Set: N:\CRF4\11072006\J552909A.raw

L:25 M:284 W: Blank Line not Allowed, <310> field identifier
L:27 M:256 W: Invalid Numeric Header Field, Wrong PUBLICATION DATE:YYYY-MM-DD
L:146 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:7
L:146 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:161 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:8
L:161 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:183 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:9
L:183 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:240
L:183 M:112 C: (48) String data converted to lower case,
M:341 Repeated in SeqNo=9